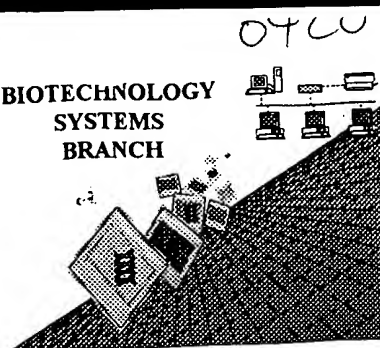


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/884,260  
Source: OPE  
Date Processed by STIC: 7/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/884,260

DATE: 07/06/2001

TIME: 11:38:51

Input Set : A:\W054316.txt

Output Set: N:\CRF3\07062001\I884260.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Alan Brash  
5 Nathalie Tijet  
8 <120> TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE  
9 LYASE AND USES THEREOF  
12 <130> FILE REFERENCE: 06027.0002  
O/c> 14 <140> CURRENT APPLICATION NUMBER: US/09/884,260  
E--> 14 <141> CURRENT FILING DATE: 2001-06-19  
E--> 14 <160> NUMBER OF SEQ ID NOS: (57) 56 (see next page)  
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

09/884, 260

2

<210> 56  
 <211> 1715  
 <212> DNA  
 <213> Cucumis melo

*Last sequence in file*

<220> ← *insert this mandatory numeric identifier whenever* (2217, 22227, or  
 <221> misc\_feature 22237 is shown  
 <222> 1283  
 <223> n = A, T, C or G

<400> 56  
 atggctactc cttcttccct cteccctgaa cttcctctca aaccaattcc cgggtggctat 60  
 ggcttccccc tcttcgggtc catcaaagac cgttacgatt acttctattt ccaaggtaga 120  
 gacgaattct tccgttcccg gattaccaaa tacaactcca ccgtcttccg cgccaacatg 180  
 ccaccggggc ccttcatttc ctccgattcc agagtcgttg tcttctcga tgccctcagt 240  
 tttcctatcc tcttcgacac agccaaagtc gagaaacgca acattctcga cggaacttac 300  
 atgccctcct tgtccttcac cggcaacatt cgcacctgtg cttatttggg cccatcggaa 360  
 acagagcact ctgttctcaa acgcctcttc ctctccttcc tgccttcccg ccatgacagg 420  
 ttcatccctc tgtttcgaag ctcttctgtc gagatgtttg ttaagcttga agataaactt 480  
 tccgagaaaa agaagatcgc tgatttcaac tcatcagcgc attccatgtc gtttgattat 540  
 gttttccgtt tactctccga tggaaacctt gattcgaat tagctgctga gggacctgga 600  
 atgttcgata tgttggttgt gtttcaactc gccccattgg cttccattgg ccttcccaaa 660  
 attttctctg tttttgaaga tctcgtcatt cacaccattc ccttgccctt cttcccagtc 720  
 aagagtgggt acaggaagct ttatgaagcg ttttactcct cttctggctc atttctagac 780  
 gaagcagaga aacaggggat agacagggag aaagcatgtc acaatttagt gtttctcgct 840  
 ggattcaacg catacggggg aatgaaagtc ctttttccca ctttactgaa atgggtcggc 900  
 accgccggcg aggatctcca ccggaactc gccgaggaag tcaggacaac cgtgaaggaa 960  
 gaagggggac tgactttctc cgccttggag aaaatgagtc tgctgaagtc cgtcgtgtac 1020  
 gaagcactca ggatcgaacc gccggtgccg ttccagtacg ggaaagcgaa ggaggatata 1080  
 gtgattcaga gccacgattc ttctttcaag atcaaaaaag gggagacgat ttttggttat 1140  
 cagccgtttg ctactaaaga tccgaagatt ttttaaggatt cggagaagtt cgtgggcgat 1200  
 aggttcgtgg gagaagaagg ggagaagctt ttgaagtatg tttactggtc aaatgagcgg 1260  
 gagacagtgg agccgacgcg gangaacaag cagtgtccgg ggaagaatct ggtggtgctg 1320  
 ataggttaga ttatgggtgt ggaattcttc cttcgttatg atacgttcac cgtggaggtc 1380  
 gcggatttgc cgtcgggtcc ggcagtgaag ttcaagtcct taaccagagc aaccgatatg 1440  
 ttaaagctaa tgactaatta gttttatcat ttacagatag tgaattgggt gatgcacgga 1500  
 agctgtggcg gactgcgcac acatgattga gtacttgggg ttattaaagt aatttcgttg 1560  
 tgatccacgt ggtcttattt taatttgaga tctcattgtg tgttgtaacc caccggtcat 1620  
 cttattttat agtttggttg ttttctcaat tatgtctcaa attttaaaat aaataaatac 1680  
 catcttcttc ttttactaaa aaaaaaaaaa aaaaaa 1715

*same  
 error  
 appears  
 in seq. 15*

*FyB*

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/884,260

DATE: 07/06/2001  
TIME: 11:38:52

Input Set : A:\W054316.txt  
Output Set: N:\CRF3\07062001\I884260.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:334 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15  
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1326 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:56  
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56  
L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (57) Counted (56)